SEQUENCE LISTING

<110> Bachmann, Martin F Tissot, Alain Pumpens, Paul Cielens, Indulis Renhofa, Regina

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<150> US 60/396,126 <151> 2002-07-17

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<170> PatentIn version 3.2

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Gly Gln Tyr Val Ser Val Tyr Lys Arg Pro Ala Pro Lys Pro Glu Gly 50 60

Cys Ala Asp Ala Cys Val Ile Met Pro Asn Glu Asn Gln Ser Ile Arg 65 70 75 80

Thr Val Ile Ser Gly Ser Ala Glu Asn Leu Ala Thr Leu Lys Ala Glu 85 90 95

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Leu Arg Gln Arg Val Lys Val Gly Ile Ala Glu Leu Asn Asn Val Ser 35 40 45

Gly Gln Tyr Val Ser Val Tyr Lys Arg Pro Ala Pro Lys Pro Glu Gly 50 60

Cys Ala Asp Ala Cys Val Ile Met Pro Asn Glu Asn Gln Ser Ile Arg 65 70 75 80

Thr Val Ile Ser Gly Ser Ala Glu Asn Leu Ala Thr Leu Lys Ala Glu 85 90 95

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00500	55555555-5-5 5 55 55	
ag		62
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      (10)..(10)
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                                                        15
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<213> Homo sapiens
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Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu
Tyr Pro Ser Ser Lys His Gln His Lys Lys
           20
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                5
Asn Pro Gln Ala Glu Gly Gln
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Pro Gln Ala Glu Gly Gln Gly Cys
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atc gaa ggt cgc aag ctt act cac aca tgc cca ccg tgc cca gca cct
                                                                       96
Ile Glu Gly Arg Lys Leu Thr His Thr Cys Pro Pro Cys Pro Ala Pro
            20
                                                                      144
gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag
Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        35
                            40
                                                                      192
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    50
                                                                      240
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
65
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac
                                                                      288
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
                                    90
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac
                                                                      336
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            100
                                105
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc
                                                                      384
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
cca gcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga
                                                                      432
Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
                        135
                                            140
    130
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aac cag gtc a Asn Gln Val S							_	528
atc gcc gtg g Ile Ala Val G 1	ag tgg gag lu Trp Glu 80	agc aat Ser Asn	ggg cag Gly Gln 185	ccg gag Pro Glu	aac aac Asn Asn 190	tac Tyr	aag Lys	576
acc acg cct c Thr Thr Pro P 195	cc gtg ttg Pro Val Leu	gac tcc Asp Ser 200	gac ggc Asp Gly	tcc ttc Ser Phe	ttc ctc Phe Leu 205	tac Tyr	agc Ser	624
aag ctc acc g Lys Leu Thr V 210	tg gac aag al Asp Lys	agc agg Ser Arg 215	tgg cag Trp Gln	cag ggg Gln Gly 220	aac gtc Asn Val	ttc Phe	tca Ser	672
tgc tcc gtg a Cys Ser Val M 225								720
ctc tcc ctg t Leu Ser Leu S		_	:					745
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Ile Glu Gly A	arg Lys Leu 20	Thr His	Thr Cys 25	Pro Pro	Cys Pro 30	Ala	Pro	
Glu Ala Glu G 35	Gly Ala Pro	Ser Val 40	Phe Leu	Phe Pro	Pro Lys 45	Pro	Lys	
Asp Thr Leu M 50	Met Ile Ser	Arg Thr 55	Pro Glu	Val Thr 60	Cys Val	Val	Val	
Asp Val Ser H	His Glu Asp 70	Pro Glu	Val Lys	Phe Asn 75	Trp Tyr	Val	Asp 80	

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 85 90 95

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp 100 105 110

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu 115 120 125

Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 130 135 140

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys 145 150 155 160

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp 165 170 175

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 180 185 190

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 195 200 205

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser 210 215 220

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 225 230 235 240

Leu Ser Leu Ser Pro Gly Lys 245

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gac gat gac gac aag ctt act cac aca tgc cca ccg tgc cca gca cct Asp Asp Asp Asp Lys Leu Thr His Thr Cys Pro Pro Cys Pro Ala Pro 20 25 30 48

96

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                                   10
Asp Asp Asp Lys Leu Thr His Thr Cys Pro Pro Cys Pro Ala Pro
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                                                                     48
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Trp Val Pro
               5
                                   10
ggt tcc act ggt gac gcg gat cca gca gct ggg ctc gag gtg cta gcg
                                                                     96
Gly Ser Thr Gly Asp Ala Asp Pro Ala Ala Gly Leu Glu Val Leu Ala
           20
gga ggg ggt gga tgt ggg gac gat gac gac aag ctt act cac aca tgc
                                                                    144
Gly Gly Gly Cys Gly Asp Asp Asp Lys Leu Thr His Thr
        35
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                                   10
                5
Gly Ser Thr Gly Asp Ala Asp Pro Ala Ala Gly Leu Glu Val Leu Ala
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20

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gtc cct gaa ctg ctg ggc tcc agc atg cca ctg tgt ccc atc gat gaa
                                                                      99
Val Pro Glu Leu Leu Gly Ser Ser Met Pro Leu Cys Pro Ile Asp Glu
                    20
gcc atc gac aag aag atc aaa caa gac ttc aac tcc ctg ttt cca aat
                                                                     147
Ala Ile Asp Lys Lys Ile Lys Gln Asp Phe Asn Ser Leu Phe Pro Asn
                35
gca ata aag aac att ggc tta aat tgc tgg aca gtc tcc tcc aga ggg
                                                                     195
Ala Ile Lys Asn Ile Gly Leu Asn Cys Trp Thr Val Ser Ser Arg Gly
            50
aag ttg gcc tcc tgc cca gaa ggc aca gca gtc ttg agc tgc tcc tgt
                                                                     243
Lys Leu Ala Ser Cys Pro Glu Gly Thr Ala Val Leu Ser Cys Ser Cys
        65
                            70
                                                                     291
ggc tct gcc tgt ggc tcg tgg gac att cgt gaa gaa aaa gtg tgt cac
Gly Ser Ala Cys Gly Ser Trp Asp Ile Arg Glu Glu Lys Val Cys His
    80
tgc cag tgt gca agg ata gac tgg aca gcc cgc tgc tgt aag ctg
                                                                     339
Cys Gln Cys Ala Arg Ile Asp Trp Thr Ala Ala Arg Cys Cys Lys Leu
95
cag gtc gct tcc tct cta gcg gga ggg ggt gga tgt ggg atc gaa ggt
                                                                     387
Gln Val Ala Ser Ser Leu Ala Gly Gly Gly Cys Gly Ile Glu Gly
                115
                                                                     399
cgc aag ctt act
Arg Lys Leu Thr
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Glu Leu Leu Gly Ser Ser Met Pro Leu Cys Pro Ile Asp Glu Ala Ile 20 25 30

Asp Lys Lys Ile Lys Gln Asp Phe Asn Ser Leu Phe Pro Asn Ala Ile 35 40 45

Lys Asn Ile Gly Leu Asn Cys Trp Thr Val Ser Ser Arg Gly Lys Leu 50 55 60

Ala Ser Cys Pro Glu Gly Thr Ala Val Leu Ser Cys Ser Cys Gly Ser 65 70 75 80

Ala Cys Gly Ser Trp Asp Ile Arg Glu Glu Lys Val Cys His Cys Gln
85 90 95

Cys Ala Arg Ile Asp Trp Thr Ala Ala Arg Cys Cys Lys Leu Gln Val 100 105 110

Ala Ser Ser Leu Ala Gly Gly Gly Gly Cys Gly Ile Glu Gly Arg Lys 115 120 125

Leu Thr 130

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1 5 10

99

gtc cct gaa ctg ctg ggc tcc agc atg cca ctg tgt ccc atc gat gaa Val Pro Glu Leu Leu Gly Ser Ser Met Pro Leu Cys Pro Ile Asp Glu 15 20 25 30

gcc atc gac aag aag atc aaa caa gac ttc aac tcc ctg ttt cca aat
Ala Ile Asp Lys Lys Ile Lys Gln Asp Phe Asn Ser Leu Phe Pro Asn

35 40 45 195 gca ata aag aac att ggc tta aat tgc tgg aca gtc tcc tcc aga ggg Ala Ile Lys Asn Ile Gly Leu Asn Cys Trp Thr Val Ser Ser Arg Gly 50 55 aag ttg gcc tcc tgc cca gaa ggc aca gca gtc ttg agc tgc tcc tgt 243 Lys Leu Ala Ser Cys Pro Glu Gly Thr Ala Val Leu Ser Cys Ser Cys 291 ggc tct gcc tgt ggc tcg tgg gac att cgt gaa gaa aaa gtg tgt cac Gly Ser Ala Cys Gly Ser Trp Asp Ile Arg Glu Glu Lys Val Cys His 85 tgc cag tgt gca agg ata gac tgg aca gcc cgc tgc tgt aag ctg 339 Cys Gln Cys Ala Arg Ile Asp Trp Thr Ala Ala Arg Cys Cys Lys Leu 100 cag gtc gct tcc tct cta gcg gga ggg ggt gga tgt ggg gac gat gac 387 Gln Val Ala Ser Ser Leu Ala Gly Gly Gly Cys Gly Asp Asp Asp 115 120 399 gac aag ctt act Asp Lys Leu Thr 130 <210> 112 130 <211> <212> PRT <213> Artificial Sequence <220> <223> Res-C-EK <400> 112 Met Lys Asn Leu Ser Phe Pro Leu Leu Phe Leu Phe Phe Leu Val Pro 5 Glu Leu Leu Gly Ser Ser Met Pro Leu Cys Pro Ile Asp Glu Ala Ile 20 Asp Lys Lys Ile Lys Gln Asp Phe Asn Ser Leu Phe Pro Asn Ala Ile 35 Lys Asn Ile Gly Leu Asn Cys Trp Thr Val Ser Ser Arg Gly Lys Leu 50 Ala Ser Cys Pro Glu Gly Thr Ala Val Leu Ser Cys Ser Cys Gly Ser 65 Ala Cys Gly Ser Trp Asp Ile Arg Glu Glu Lys Val Cys His Cys Gln 90

Cys Ala Arg Ile Asp Trp Thr Ala Ala Arg Cys Cys Lys Leu Gln Val

100 105 110

Ala Ser Ser Leu Ala Gly Gly Gly Gly Cys Gly Asp Asp Asp Lys 125 115 120

Leu Thr 130

<210> 113

<211> 26 <212> PRT <213> Mus musculus

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Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp Phe Thr Trp His 10

Ser Pro Pro Ser Lys Ser His His Lys Lys

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<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> rat MIF-C1

<400> 114

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Glu

Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys

Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Thr

Phe Ser Gly Thr Ser Asp Pro Cys Ala Leu Cys Ser Leu His Ser Ile

Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu Cys

Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr Ile 90

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser Thr 100 105 110

Phe Ala Gly Gly Gly Gly Cys Gly 115 120

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<400> 115

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Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Thr 35 40 45

Phe Ser Gly Thr Ser Asp Pro Cys Ala Leu Cys Ser Leu His Ser Ile 50 60

Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu Cys 65 70 75 80

Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr Ile 85 90 95

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser Thr
100 105 110

Phe Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly Gly Ala Pro 115 120 125

Gly Gly Cys Gly 130

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Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly Gly Ala Pro Gly Gly

15 5 10 Cys Gly <210> 117 <211> 124 <212> PRT <213> Artificial Sequence <220> <223> rat MIF-C3 <400> 117 Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Glu 10 Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Thr 40 Phe Ser Gly Thr Ser Asp Pro Cys Ala Leu Cys Ser Leu His Ser Ile 55 Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu Cys 70 75 65 80 Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr Ile 85 95 Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser Thr 100 Phe Ala Asp Lys Thr His Thr Ser Pro Pro Cys Gly 115 120 <210> 118 <211> 10 <212> PRT <213> Artificial Sequence <223> amino acid linker C3 <400> 118 Asp Lys Thr His Thr Ser Pro Pro Cys Gly

- <210> 119 <211> 114 <212> PRT <213> Homo sapiens

<400> 119

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Asp 10

Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys 25

Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Ala

Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser Ile

Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu Cys 75

Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr Ile

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr 100 105

Phe Ala

- <210> 120
- <211> 114
- <212> PRT
- <213> Rattus norvegicus

<400> 120

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Glu 10

Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys

Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Thr 40

Phe Ser Gly Thr Ser Asp Pro Cys Ala Leu Cys Ser Leu His Ser Ile 55 60

Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu Cys 70 75 80

Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr Ile 85 90 95

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser Thr 100 105 110

Phe Ala

<210> 121

<211> 114

<212> PRT

<213> Mus musculus

<400> 121

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Glu
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Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys 20 25 30

Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Thr 35 40 45

Phe Ser Gly Thr Asn Asp Pro Cys Ala Leu Cys Ser Leu His Ser Ile 50 55 60

Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu Cys
70 75 80

Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr Ile 85 90 95

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser Thr 100 105 110

Phe Ala

<210> 122

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> human MIF-C1

<400> 122

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Asp 1 5 10 15

Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys 20 25 30

Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Ala 35 40 45

Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser Ile 50 55 60

Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu Cys 65 70 75 80

Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr Ile 85 90 95

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr 100 105 110

Phe Ala Gly Gly Gly Cys Gly

<210> 123

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> human MIF-C2

<400> 123

Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Asp 1 5 10 15

Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys 20 25 30

Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Ala 35 40 45

Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser Ile 50 55 60

Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu Cys 65 70 75 80 Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr Ile 85 90 95

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr 100 105 110

Phe Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Gly Gly Ala Pro

Gly Gly Cys Gly 130

<210> 124

<211> 124

<212> PRT

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<223> human MIF-C3

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Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Asp 1 5 10 15

Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys 20 25 30

Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Ala 35 40 45

Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser Ile 50 55 60

Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu Cys 65 70 75 80

Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr Ile 85 90 95

Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr 100 105 110

Phe Ala Asp Lys Thr His Thr Ser Pro Pro Cys Gly

<210> 125

<211> 396

<212> DNA

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<400>	125								
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ccaact	egtt	tatcaactac	attttcagca	agtctgttac	gccaacgtgt	taaagttggt	120		
atagcc	gaac	tgaataatgt	ttcaggtcaa	tatgtatctg	tttataagcg	tcctgcacct	180		
aaaccg	gaag	gttgtgcaga	tgcctgtgtc	attatgccga	atgaaaacca	atccattcgc	240		
acagtga	attt	cagggtcagc	cgaaaacttg	gctaccttaa	aagcagaatg	ggaaactcac	300		
aaacgta	aacg	ttgacacact	cttcgcgagc	ggcaacgccg	gtttgggttt	ccttgaccct	360		
actgcgg	gcta	tcgtatcgtc	tgatactact	gcttaa			396		